



500

Figure S3. Phylogenetic trees based on 32 concatenated proteins of *Mollicutes*. The tree was generated from a multiple sequence alignment using neighbor-joining (shown) and maximum likelihood (not shown) algorithms with 1,000 bootstrap replicates. *Bacillus subtilis* subsp. *subtilis* str. 168 was used as outgroup. All branches agree with those constructed using the maximum likelihood method. Bar shows substitution per nucleotide.